STIC-Biotech/ChemLib 96054

From: Prouty, Rebecca
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Art Unit 1652, 10A13
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Mary Jane Ruhl
Tech. Info. Specialist, STIC
TC-1600
CM-1, Room 6A-06
Phone: 605-1155

	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher:_____	NA Sequences:_____	STN:_____
Phone:_____	AA Sequences:_____	DIALOG:_____
Location:_____	Structures:_____	Questel/Orbit:_____
Date Picked Up:_____	Bibliographic:_____	DRLink:_____
Date Completed:_____	Litigation:_____	Lexis/Nexis:_____
Searcher Prep/Review:_____	Full text:_____	Sequence Sys.:_____
Clerical:_____	Patent Family:_____	WWW/Internet:_____
Online time:_____	Other:_____	Other (specify):_____

	L #	Hits	Search Text	DBs	Time Stamp
1	L1	9242	esterase$1	USPAT; US-PGPUB	2003/06/06 15:06
2	L2	116	aquifex or pyrophilus	USPAT; US-PGPUB	2003/06/06 15:08
3	L3	22	1 and 2	USPAT; US-PGPUB	2003/06/06 15:29
4	L4	5	1 same 2	USPAT; US-PGPUB	2003/06/06 15:29

PGPUB-DOCUMENT-NUMBER: 20030064491

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030064491 A1

TITLE: Genes and proteins involved in the biosynthesis of enediyne ring structures

PUBLICATION-DATE: April 3, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Farnet, Chris M.	Outremont		CA	
Staffa, Alfredo	Saint-Laurent		CA	
Zazopoulos, Emmanuel	Montreal		CA	

APPL-NO: 10/ 152886

DATE FILED: May 21, 2002

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60291959 20010521 US

non-provisional-of-provisional 60334604 20011203 US

US-CL-CURRENT: 435/183, 435/320.1 , 435/325 , 435/69.1 , 435/76 , 536/23.2

ABSTRACT:

Five protein families cooperate to form the warhead structure that characterizes enediyne compounds, both chromoprotein enediynes and non-chromoprotein enediynes The protein families include a polyketide synthase and thioesterase protein which form a polyketide synthase catalytic complex involved in warhead formation in enediynes. Genes encoding a member of each of the five protein families are found in all enediyne biosynthetic loci. The genes and proteins may be used in genetic engineering applications to design new enediyne compounds and in methods to identify new enediyne biosynthetic loci.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims benefit under 35 USC .sctn. 119 of provisional applications U.S. Ser. No. 60/291,959 filed on May 21, 2001 and U.S. Ser. No. 60/334,604 filed on Dec. 3, 2001 which are hereby incorporated by reference in their entirety for all purposes.

---------- KWIC ---------

Detail Description Table CWU - DETL (11):

11TABLE 10 135E locus GenBank homology proposed function of Family #aa Accession, #aa probability identity similarity GenBank match PKSE 1933 T37056, 2082aa 1e-65 282/909 (31.02%) 365/909 (40.15%) multi-domain beta keto-acyl synthase, Streptomyces coelicolor BAB69208 1, 2365aa 3e-84 285/925 (30.81%) 366/925 (39.57%) polyketide synthase, Streptomyces avermitilis T30937, 1053aa 2e-69 246/907 (27.12%) 356/907 (39.25%) glycolipid synthase, Nostoc punctiforme TEBC 154 NP_249659 1, 146aa 2e-07 41/132 (31.06%) 63/132 (47.73%) hypothetical protein, Pseudomonas aeruginosa AAD49752 1, 148aa 2e-06 40/132 (30.3%) 62/132 (46.97%) orf1, Pseudomonas aeruginosa NP_214031 1, 128aa 5e-04 35/127 (27.56%) 60/127 (47.24%) hypothetical protein, **Aquifex** aeolicus UNBL 323 NO HOMOLOG UNBV 655 CAC44518 1, 706aa 9e-04 41/135 (30.37%) 59/135 (43.7%) putative secreted **esterase,** Streptomyces coelicolor UNBU 346 NP_486037 1, 300aa 4e-09 52/191 (27.23%) 87/191 (45.55%) hypothetical protein, Nostoc sp NP_440874 1, 285aa 9e-06 47/197 (23.86%) 89/197 (45.18%) hypothetical protein, Synechocystis sp

PGPUB-DOCUMENT-NUMBER: 20030054530

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030054530 A1

TITLE: Esterases

PUBLICATION-DATE: March 20, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Robertson, Dan E.	Solana Beach	CA	US	
Murphy, Dennis	Malvern	PA	US	
Reid, John	Ardmore	PA	US	
Maffia, Anthony M.	Old Bridge	NJ	US	
Link, Steven	Wilmington	DE	US	
Swanson, Ronald V.	Del Mar	CA	US	
Warren, Patrick V.	Coatesville	PA	US	
Lenox, Anna	Perkiomenville	PA	US	
Short, Jay M.	Rancho Santa Fe	CA	US	
Mathur, Eric J.	Carlsbad	CA	US	

APPL-NO: 10/ 027804

DATE FILED: December 21, 2001

RELATED-US-APPL-DATA:

child 10027804 A1 20011221

parent division-of 09903410 20010710 US PENDING

child 09903410 20010710 US

parent continuation-in-part-of 09382242 19990824 US PENDING

child 09382242 19990824 US

parent continuation-of 08602359 19960216 US GRANTED

parent-patent 5942430 US

US-CL-CURRENT: 435/196

ABSTRACT:

Esterase enzymes derived from various Staphylothermus, Pyrodictium, Archaeoglobus, Aquifex, **M11TL, T**hermococcus, Teredinibacter and Sulfolobus organisms are disclosed. The enzymes are produced from native or recombinant host cells and can be utilized in pharmaceutical, agricultural and other

industries.

RELATED APPLICATIONS

[0001] This application is a divisional of co-pending U. S. patent application Ser. No. 08/602,359, filed Feb. 17, 1996.

---------- KWIC ---------

Abstract Paragraph - ABTX (1):

Esterase enzymes derived from various Staphylothermus, Pyrodictium, Archaeoglobus, **Aquifex,** M11TL, Thermococcus, Teredinibacter and Sulfolobus organisms are disclosed. The enzymes are produced from native or recombinant host cells and can be utilized in pharmaceutical, agricultural and other industries.

PGPUB-DOCUMENT-NUMBER: 20020164725

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020164725 A1

TITLE: Esterases

PUBLICATION-DATE: November 7, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Robertson, Dan E.	Solana Beach	NJ	US	
Murphy, Dennis	Malvern	PA	US	
Reid, John	Armore	PA	US	
Maffia, Anthony	Wilmington	DE	US	
Link, Steven	Wilmington	DE	US	
Swanson, Ronald V.	Del Mar	CA	US	
Warren, Patrick V.	Coatesville	PA	US	
Kosmatka, Anna	Doylestown	PA	US	

APPL-NO: 10/ 027805

DATE FILED: December 21, 2001

RELATED-US-APPL-DATA:

child 10027805 A1 20011221

parent division-of 09903410 20010710 US PENDING

child 09903410 20010710 US

parent continuation-in-part-of 09382242 19990824 US PENDING

child 09382242 19990824 US

parent continuation-of 08602359 19960216 US GRANTED

parent-patent 5942430 US

US-CL-CURRENT: 435/106

ABSTRACT:

Esterase enzymes derived from various Staphylothermus, Pyrodictium, Archaeoglobus, Aquifex, **M11TL, T**hermococcus, Teredinibacter and Sulfolobus organisms are disclosed. The enzymes are produced from native or recombinant host cells and can be utilized in pharmaceutical, agricultural and other industries.

RELATED APPLICATIONS

[0001] This application is a divisional of co-pending U.S. patent application Ser. No. 08/602,359, filed Feb. 17, 1996.

---------- KWIC ---------

Abstract Paragraph - ABTX (1):

Esterase enzymes derived from various Staphylothermus, Pyrodictium, Archaeoglobus, **Aquifex,** M11TL, Thermococcus, Teredinibacter and Sulfolobus organisms are disclosed. The enzymes are produced from native or recombinant host cells and can be utilized in pharmaceutical, agricultural and other industries.

US-PAT-NO: 6562958

DOCUMENT-IDENTIFIER: US 6562958 B1

TITLE: Nucleic acid and amino acid sequences relating to Acinetobacter baumannii for diagnostics and therapeutics

DATE-ISSUED: May 13, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Breton; Gary	Marlborough	MA	N/A	N/A
Bush; David	Somerville	MA	N/A	N/A

APPL-NO: 09/ 328352

DATE FILED: June 4, 1999

PARENT-CASE:

RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No. 60/088,701, filed Jun. 9, 1998, the entire teachings of which are incorporated herein by reference.

US-CL-CURRENT: 536/23.7, 536/23.1

ABSTRACT:

The invention provides isolated polypeptide and nucleic acid sequences derived from Acinetobacter mirabilis that are useful in diagnosis and therapy of pathological conditions; antibodies against the polypeptides; and methods for the production of the polypeptides. The invention also provides methods for the detection, prevention and treatment of pathological conditions resulting from bacterial infection.

15 Claims, 0 Drawing figures

Exemplary Claim Number: 1

---------- KWIC ---------

Detailed Description Paragraph Table - DETL (77):
AMINOBENZOATE SYNTHASE COMPONENT I, (ADC SYNTHASE)] [SP:P05041] Contig140G 1361583_c1_62 1857 5983 696 231 468 1.90E-44 sp:[LN:HISI_BACSU] [AC:034520] [GN:HISG] [OR:BACILLUS SUBTILIS] [EC:2.4.2.17] [DE:ATP PHOSPHORIBOSYLTRANSFER ASE,] [SP:034520] Contig140G 1443927_c1_72 1858 5984

681 226 343 3.30E-31 sp:[LN:YEAZ_ECOLI] [AC:P76256:O08476:O08477] [GN:YEAZ] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL 25.2 KD PROTEIN IN FADD- PABB INTERGENIC REGION] [SP:P76256:O08476:O08477] Contig140G 19800062_f1_9 1859 5985 591 196 425 6.70E-40 gp:[GI:g1871177] [LN:ATU90439] [AC:U90439] [GN:T06D20.4] [OR:Arabidopsis thaliana] [SR:thale cress] [DE:Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence,complete sequence.] [NT:unknown protein] Contig140G 20744002_c2_85 1860 5986 534 177 481 7.80E-46 sp:[LN:FBP_PSEAE] [AC:P40882] [GN:FBP] [OR:PSEUDOMONAS AERUGINOSA] [DE:FERRIPYOCHELIN BINDING PROTEIN] [SP:P40882] Contig140G 22689193_c3_97 1861 5987 1677 558 80 9.30E-05 pir:[LN:H70355] [AC:H70355] [PN:hypothetical protein aq_627] [GN:aq_627] [OR:**Aquifex** acolicus] Contig140G 23703138_c2_88 1862 5988 849 282 581 2.00E-56 pir:[LN:F64819] [AC:F64819] [PN:hypothetical protein b0822] [OR:Escherichia coli] Contig140G 23853200_c2_90 1863 5989 837 278 223 1.80E-18 pir:[LN:B36868] [AC:B36868] [PN:copB homolog:hypotheticalprotein 2] [OR:Xanthomonas campestris] Contig140G 24407827_c3_99 1864 5990 1926 641 NO-HIT Contig140G 24431540_c3_102 1865 5991 843 280 294 5.10E-26 sp:[LN:YHIQ_NEIGO] [AC:P72077] [OR:NEISSERIA GONORRHOEAE] [DE:HYPOTHETICAL 27.3 KD PROTEIN] [SP:P72077] Contig140G 24662562_c2_91 1866 5992 336 111 301 9.30E-27 sp:[LN:SUGE_CITFR] [AC:O69279] [GN:SUGE] [OR:CITROBACTER FREUNDII] [DE:SUGE PROTEIN HOMOLOG] [SP:O69279] Contig140G 258442_c1_76 1867 5993 1056 352 1240 2.90E-126 sp:[LN:NADA_ECOLI] [AC:P11458:P77373] [GN:NADA:NICA] [OR:ESCHERICHIA COLI] [DE:QUINOLINATE SYNTHETASE A] [SP:P11458:P77373] Contig140G 26259753_c2_79 1868 5994 273 90 373 2.20E-34 sp:[LN:YRPM_ACICA] [AC:P33989] [OR:ACINETOBACTER CALCOACETICUS] [DE:HYPOTHETICAL 9.2 KD PROTEIN IN RPON-MURA INTERGENIC REGION (ORF3)] [SP:P33989] Contig140G 26350790_c1_63 1869 5995 1353 450 1024 2.20E-103 pir:[LN:E70368] [AC:E70368] [PN:histidinol dehydrogenase] [GN:hisD] [CL:histidinol dehydrogenase:histidinol dehydrogenase homology] [OR:**Aquifex** aeolicus] Contig140G 26579061_c2_93 1870 5996 1242 413 1013 3.30E-102 sp:[LN:ARGJ_NEIGO] [AC:P38434] [GN:ARGJ] [OR:NEISSERIA GONORRHOEAE] [EC:2.3.1.35:2.3.1.1] [DE:ACETYLTRANSFERASE, (N-ACETYLGLUTAMATE SYNTHASE)(AGS)] [SP:P38434] Contig140G 26600052_c2_80 1871 5997 1263 420 1928 3.60E-199 sp:[LN:MURA_ACICA] [AC:P33986] [GN:MURA:MURZ] [OR:ACINETOBACTER CALCOACETICUS] [EC:2.5.1.7] [DE:TRANSFERASE)(EPT)] [SP:P33986] Contig140G 2853452_c3_104 1872 5998 399 132 NO-HIT Contig140G 29485012_c3_106 1873 5999 1032 343 174 8.50E-13 gp:[GI:e258655:g1628369] [LN:DNINTREG] [AC:X98546] [GN:gepB] [OR:Dichelobacter nodosus] [DE:D.nodosus intB, regA, gepA, gepB, and gepC genes.] Contig140G 30704408_c1_75 1874 6000 573 190 356 1.40E-32 gp:[GI:e1370607:g4158208] [LN:SC9B5] [AC:AL035206] [PN:putative methylated-DNA- protein-cysteine] [GN:SC9B5.29] [OR:Streptomyces coelicolor] [DE:Streptomyces coelicolor] cosmid 9B5.] [NT:SC9B5.29, ogt2, methylated-DNA-protein- cysteine] Contig140G 31822052_c3_98 1875 6001 192 63 112 9.90E-07 pir:[LN:S66936] [AC:S66936:S662927] [PN:probable membrane protein YOR053w:hypothetical protein O2799] [OR:Saccharomyces cerevisiae] [MP:15R] Contig140G 33618802_c2_87 1876 6002 882 293 725 1.10E-71 sp:[LN:ESTD_HUMAN] [AC:P1O768] [GN:ESD] [OR:HOMO SAPIENS] [EC:3.1.1.1] [DE:**ESTERASE** D,] [SP:P 0768] Contig140G 35267331_c1_74 1877 6003 2016 671 1238 4.70E-126 pir:[LN:A36868] [AC:A36868] [PN:copA homolog:hypothetical protein 1] [CL:laccase] [OR:Xanthomonas campestris] Contig140G 35781253_f1_10 1878 6004 261 86 119 1.80E-07 pir:[LN:S56703] [AC:S56703] [PN:glycine-rich cell wall protein precursor:CEM6 protein] [OR:Daucus carota] [SR:, carrot] Contig140G 35948293_c3_95 1879 6005 867 288 128 6.80E-08 pir:[LN:H69061]

[AC:H69061] [PN:ABC transporter related

Detailed Description Paragraph Table - DETL (141):
[AC:P37764] [GN:YAEL] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL 49.1 KD PROTEIN IN CDSA-HLPA INTERGENIC REGION] [SP:P37764] Contig151G 4101588_f3_442 3347 7473 1062 353 941 1.40E-94 gp:[GI:d1033097:g3401952) [LN:AB011413] [AC:AB011413] [PN:Orf8] [FN:alcohol dehydrogenase] [OR:Streptomyces griseus] [SR:Streptomyces griseus DNA] [DE:Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8,partial and complete cds.] Contig151G 4103461_c3_1036 3348 7474 897 298 318 1.50E-28 gp:[GI:g3660461] [LN:PSAF001355] [AC:AF001355:U16026:U03465: U87170] [PN:DNA binding protein HpkR] [GN:hpkR] [OR:Pseudomonas syringae pv. syringae] [DE:Pseudomonas syringae pv. syringae DNA binding protein HpkR (hpkR),hybrid histidine protein kinase-phosphate acceptor regulatoryprotein CvgSY (cvgSY), ankyrin AnkF (ankF), and catalase isozymecatalytic subunit CatF (catF) genes, complete cds.] [NT:similarity suggests this is a member of the HTH] Contig151G 4103462_c2_724 3349 7475 1581 526 351 2.30E-30 gp:]GI;g3414726] [LN:AF047693] [AC:AF047693] [PN:multidrug resistance efflux pump homolog PmrB] [GN:pmrB] [OR:Pseudomonas aeruginosa] [DE:Pseudomonas aeruginosa multidrug resistance efflux pump homologPmrA (pmrA) and multidrug resistance efflux pump homolog PmrB(mmrB) genes, complete cds.] [NT:14 TMS efflux pump; similar to EmrB of Escherichia] Contig151G 4105312_f3_402 3350 7476 375 124 NO-HIT Contig151G 4110142_c2_814 3351 7477 558 185 120 1.40E-07 gp:[GI:g4139249] [LN:AF110185] [AC:AF110185] [PN:unknown] [OR:Burkholderia pseudomallei] [DE:Burkholderia pseudomallei strain 1026b DbhB (dbhB), generalsecretory pathway protein D (gspD), general secretory pathwayprotein E (gspE), general secretory pathway protein F (gspF), GspC(gspC), general secretory pathway protein G (gspG), generalsecretory pathway protein H (gspH), general secretory pathwayprotein I (gsp1), general secretory pathway protein J (gspJ),general secretory pathway protein K (gspK), general secretorypathway protein L (gspL), general secretory pathway protein M(gspM), and general secretory pathway protein N (gspN) genes,complete cds; and unknown genes.] [NT:similar to Escherichia coli MarR protein; orfE] Contig151G 4118800_f1_63 3352 7478 1104 367 304 4.50E-27 gp:[GI:g2852632] [LN:AF007152] [AC:AF007152] [PN:unknown] [OR:Homo sapiens] [DE:Homo sapiens clone 23649 and 23755 unknown mRNA, partial cds.] Contig151G 4140712_c2_739 3353 7479 336 111 114 6.10E-07 sp:[LN:YH83_SYNY3] [AC:P73602] [GN:SLL1783] [OR:SYNECHOCYSTIS SP] [SR:PCC 6803,] [DE:HYPOTHETICAL 16.8 KD PROTEIN SLL1783] [SP:P73602] Contig151G 4142840_f2_257 3354 7480 528 175 NO-HIT Contig151G 4147318_c2_733 3355 7481 1350 449 923 1.10E-92 sp:[LN:TUB3_AGRVI] [AC:P70786] [GN:TTUB] [OR:AGROBACTERIUM VITIS] [DE:PUTATIVE TARTRATE TRANSPORTER] [SP:P70786] Contig151G 4156377_c2_174 3356 7482 891 296 877 8.50E-88 pir:[LN:E69778] [AC:E69778] [PN:conserved hypothetical protein ydeK] [GN:ydeK] [OR:Bacillus subtilis] Contig151G 42087_f1_88 3357 7483 858 285 1169 970E-119 pir:[LN:JC4161] [AC:JC4161:PC4038] [PN:probable chloride peroxidase,**:esterase** (misidentification)] [CL:peroxidase] [OR:Pseudomonas putida] [EC:1.11.1.10] Contig151G 4335950_f2_156 3358 7484 1155 384 138 5.40E-07 pir:[LN:E70470] [AC:E70470] [PN:conserved hypothetical protein aq_1986] [GN:aq_1986] [OR:**Aquifex** aeolicus] Contig151G 4339132_c1_621 3359 7485 639 212 133 1.50E-07 pir:[LN:H65092] [AC:H65092] [PN:hypothetical protein b3050] [OR:Escherichia coli] Contig151G 4344568_c1_568 3360 7486 816 271 337 1.40E-30 pir:[LN:S69588] [AC:S69588] [PN:hypothetical protein

YDR533c] [CL:conserved hypothetical protein YMR322c] [OR:Saccharomyces cerevisiae] [MP:4R] Contig151G 4375258_c3_994 3361 7487 1464 487 1670 7.90E-172 gp:[GI:e321556:g2208982] [LN:YEY13308] [AC:Y13308] [PN:sulfate permease] [OR:Yersinia enterocolitica] [DE:Yersinia enterocolitica plasmid DNA fragment, strain 15673.] [NT:ORF3] Contig151G 439452_f1_57 3362 7488 792 263 NO-HIT Contig151G 4398376_f1_335 3363 7489 513 170 NO-HIT Contig151G 4429088_f2_268 3364 7490 468 155 NO-HIT Contig151G 4429642_f3_419 3365 7491 1269 422 601 1.50E-58 gp:[GI:g2291144] [LN:CELF17A9] [AC:AF016417] [GN:F17A9.4]

US-PAT-NO: 5942430

DOCUMENT-IDENTIFIER: US 5942430 A

TITLE: Esterases

DATE-ISSUED: August 24, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Robertson; Dan E.	Haddonfield	NJ	N/A	N/A
Murphy; Dennis	Paoli	PA	N/A	N/A
Reid; John	Bryn Mawr	PA	N/A	N/A
Maffia; Anthony M.	Wilmington	DE	N/A	N/A
Link; Steven	Wilmington	DE	N/A	N/A
Swanson; Ronald V.	Media	PA	N/A	N/A
Warren; Patrick V.	Philadelphia	PA	N/A	N/A
Kosmotka; Anna	Brookhaven	PA	N/A	N/A

APPL-NO: 08/ 602359

DATE FILED: February 16, 1996

US-CL-CURRENT: 435/197, 435/196 , 435/252.3 , 435/320.1 , 435/325 , 536/23.2

ABSTRACT:

Esterase enzymes derived from various Staphylothermus, Pyrodictium, Archaeoglobus, **Aquifex**, M11TL, Thermococcus, Teredinibacter and Sulfolobus organisms are disclosed. The enzymes are produced from native or recombinant host cells and can be utilized in the pharmaceutical, agricultural and other industries.

9 Claims, 17 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 17

---------- KWIC ---------

Abstract Text - ABTX (1):
Esterase enzymes derived from various Staphylothermus, Pyrodictium, Archaeoglobus, **Aquifex**, M11TL, Thermococcus, Teredinibacter and Sulfolobus organisms are disclosed. The enzymes are produced from native or recombinant host cells and can be utilized in the pharmaceutical, agricultural and other industries.

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 FILE 'HOME' ENTERED AT 15:32:53 ON 06 JUN 2003

 => fil .bec
 COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                            ENTRY    SESSION
 FULL ESTIMATED COST                                         0.21       0.21

 FILES 'MEDLINE, SCISEARCH, LIFESCI, BIOTECHDS, BIOSIS, EMBASE, HCAPLUS, NTIS,
        ESBIOBASE, BIOTECHNO, WPIDS' ENTERED AT 15:33:01 ON 06 JUN 2003
 ALL COPYRIGHTS AND RESTRICTIONS APPLY.  SEE HELP USAGETERMS FOR DETAILS.

 11 FILES IN THE FILE LIST

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 FILE 'MEDLINE'
 L1        21802 ESTERASE#

 FILE 'SCISEARCH'
 L2        13059 ESTERASE#

 FILE 'LIFESCI'
 L3         5550 ESTERASE#

 FILE 'BIOTECHDS'
 L4         2087 ESTERASE#

 FILE 'BIOSIS'
 L5        43911 ESTERASE#

 FILE 'EMBASE'
 L6        14071 ESTERASE#

 FILE 'HCAPLUS'
 L7        33241 ESTERASE#

 FILE 'NTIS'
 L8          300 ESTERASE#

 FILE 'ESBIOBASE'
 L9         3414 ESTERASE#

 FILE 'BIOTECHNO'
 L10        4464 ESTERASE#

 FILE 'WPIDS'
 L11        2245 ESTERASE#

 TOTAL FOR ALL FILES
 L12      144144 ESTERASE#

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             30 PYROPHILUS
 L13        142 AQUIFEX OR PYROPHILUS

 FILE 'SCISEARCH'
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             77 PYROPHILUS
 L14        189 AQUIFEX OR PYROPHILUS

 FILE 'LIFESCI'
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             27 PYROPHILUS
L15         107 AQUIFEX OR PYROPHILUS

FILE 'BIOTECHDS'
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              7 PYROPHILUS
L16          23 AQUIFEX OR PYROPHILUS

FILE 'BIOSIS'
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             50 PYROPHILUS
L17         210 AQUIFEX OR PYROPHILUS

FILE 'EMBASE'
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             29 PYROPHILUS
L18         128 AQUIFEX OR PYROPHILUS

FILE 'HCAPLUS'
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             53 PYROPHILUS
L19         255 AQUIFEX OR PYROPHILUS

FILE 'NTIS'
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              1 PYROPHILUS
L20           1 AQUIFEX OR PYROPHILUS

FILE 'ESBIOBASE'
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             26 PYROPHILUS
L21         125 AQUIFEX OR PYROPHILUS

FILE 'BIOTECHNO'
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             29 PYROPHILUS
L22         123 AQUIFEX OR PYROPHILUS

FILE 'WPIDS'
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              8 PYROPHILUS
L23          24 AQUIFEX OR PYROPHILUS

TOTAL FOR ALL FILES
L24        1327 AQUIFEX OR PYROPHILUS

=> s l12 and l24
FILE 'MEDLINE'
L25           1 L1 AND L13

FILE 'SCISEARCH'
L26           0 L2 AND L14

FILE 'LIFESCI'
L27           0 L3 AND L15

FILE 'BIOTECHDS'
L28           2 L4 AND L16

FILE 'BIOSIS'
L29           0 L5 AND L17

FILE 'EMBASE'
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L30             0 L6 AND L18

FILE 'HCAPLUS'
L31             3 L7 AND L19

FILE 'NTIS'
L32             0 L8 AND L20

FILE 'ESBIOBASE'
L33             0 L9 AND L21

FILE 'BIOTECHNO'
L34             0 L10 AND L22

FILE 'WPIDS'
L35             1 L11 AND L23

TOTAL FOR ALL FILES
L36             7 L12 AND L24

=> dup rem l36
PROCESSING COMPLETED FOR L36
L37             4 DUP REM L36 (3 DUPLICATES REMOVED)

=> d tot

L37   ANSWER 1 OF 4  BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
TI    New isolated nucleic acid and its variants comprising specified
      consecutive amino acid sequences and corresponding cDNA sequences, encode
      polypeptides having esterase activity;
         recombinant enzyme production via plasmid expression in host cell, for
         ester hydrolysis
AU    ROBERTSON D E; MURPHY D; REID J; MAFFIA A M; LINK S; SWANSON R; WARREN P
      V; KOSMATKA A
AN    2003-07813  BIOTECHDS
PI    US 2002146799 10 Oct 2002

L37  ANSWER 2 OF 4  HCAPLUS  COPYRIGHT 2003 ACS
TI   Nucleic acids encoding human cyclic nucleotide-associated proteins
SO   PCT Int. Appl., 78 pp.
     CODEN: PIXXD2
IN   Hillman, Jennifer L.; Yue, Henry; Guegler, Karl J.; Corley, Neil C.;
     Patterson, Chandra; Tang, Y. Tom
AN   2000:175945  HCAPLUS
DN   132:218013
     PATENT NO.        KIND  DATE          APPLICATION NO.  DATE
     --------------    ----  --------      ---------------  --------
PI   WO 2000014248      A1   20000316       WO 1999-US20287  19990903
         W:  AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE,
             DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP,
             KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN,
             MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
             TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU,
             TJ, TM
         RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK,
             ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG,
             CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
     AU 9960263         A1   20000327       AU 1999-60263    19990903
     EP 1144648         A1   20011017       EP 1999-968683   19990903
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO

L37  ANSWER 3 OF 4     MEDLINE
TI   Mutational analysis of the RecJ exonuclease of Escherichia coli:
```

identification of phosphoesterase motifs.
SO JOURNAL OF BACTERIOLOGY, (1999 Oct) 181 (19) 6098-102.
Journal code: 2985120R. ISSN: 0021-9193.
AU Sutera V A Jr; Han E S; Rajman L A; Lovett S T
AN 1999429858 MEDLINE

L37 ANSWER 4 OF 4 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
TI New nucleic acid encoding heat stable **esterases** from thermophilic bacteria;
recombinant thermostable **esterases** for use in pharmaceutical, agricultural or food industries, etc.
AU Robertson D E; Murphy D; Reid J; Maffia A M; Link S; Swanson R V; Warren P V; Kosmotka A; Callen W
AN 1997-11973 BIOTECHDS
PI WO 9730160 21 Aug 1997

=> d ab tot

L37 ANSWER 1 OF 4 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
AB DERWENT ABSTRACT:
NOVELTY - Isolated nucleic acid (I) and its variants comprising consecutive amino acid sequences and corresponding cDNA sequences given in the specification, encoding a polypeptide with **esterase** activity, are new.

DETAILED DESCRIPTION - An isolated nucleic acid and its variants encoding a polypeptide with **esterase** activity comprising sequence of 185 amino acids and corresponding cDNA sequence of 555 bp, 347 amino acids and corresponding cDNA sequence of 1041 bp, 263 amino acids and corresponding cDNA sequence of 789 bp, 252 amino acids and corresponding cDNA sequence of 756 bp, 298 amino acids and corresponding cDNA sequence of 894 bp, 263 amino acids and corresponding cDNA sequence of 789 bp, 250 amino acids and corresponding cDNA sequence of 750 bp, 339 amino acids and corresponding cDNA sequence of 1017 bp, 311 amino acids and corresponding cDNA sequence of 936 bp, or 305 amino acids and corresponding cDNA sequence of 918 bp given in the specification, are new. The variants of the nucleic acid have at least50% identity to the same sequences above. INDEPENDENT CLAIMS are also included for: (1) a computer readable medium storing the specified sequences above as well as specified deduced amino acid sequences; (2) preparing a first sequence to a reference sequence comprising reading the first sequence and reference sequence through the use of computer program which compares the sequences, and determining the differences between the first sequence and reference sequence with the computer program; (3) an assay for identifying functional polypeptide fragments or variants encoded by the fragments of specified sequences above as well as specified deduced amino acid sequences, comprising contacting the polypeptide with a substrate molecule under conditions allowing the polypeptide or fragment or variant to function, and detecting if there is either decrease in the level of substrate or increase in the level of substrate reaction product of the reaction between the polypeptide and substrate; (4) a nucleic acid probe comprising oligonucleotide of 10-50 nucleotides in length and having an area of at least10 contiguous nucleotides that is at least50% complementary to the nucleic acid target region of the nucleic acid with specified sequences; (5) an enzyme preparation comprising the liquid or dry polypeptide; and (6) an antibody that specifically binds to the polypeptide.

BIOTECHNOLOGY - Preparation: The polypeptide is prepared by introducing a nucleic acid encoding the polypeptide into a host cell under conditions that allow expression of the polypeptide and recovering the polypeptide. Its variants are generated by obtaining a nucleic acid comprising the specified sequences of fragments comprising at least30 consecutive nucleotides and complementary to the above sequence, modifying nucleotides in the sequence to another nucleotide, and deleting

or adding one or more sequences in the sequence. Preferred Properties: The isolated nucleic acid hybridizes to nucleic acid under high, moderate or low stringency conditions. The nucleic acid also encodes polypeptide having deduced amino acid sequence of Staphylothermus marinus F1-12LC, deduced amino acid sequence of Pyrodictium TAGI 1-17LC, deduced amino acid sequence of Archaeoglobus venificus SNP6-24LC, deduced amino acid sequence of **Aquifex pyrophilus**-28LC, deduced amino acid sequence of M11TL-29L, deduced amino acid sequence of Thermococcus CL-2-30LC, deduced amino acid sequence of **Aquifex** VF5-34LC, deduced amino acid sequence of Teredinibacter-42L, deduced amino acid sequence of Archaeoglobus fulgidus VC16-16MC and deduced amino acid sequence of Sulfolobus solfataricus P1-8LC. The purified polypeptide has at least50 (preferably at least95)% homology to the nucleic acid as determined by analysis with a sequence comparison algorithm. The sequence comparison algorithm is FASTA version 3.0t78 with the default parameters. The antibodies may be polyclonal or monoclonal. The oligonucleotide is DNA. It has 15-50 bases in length. Preferred Components: The probe comprises a detectable isotropic label, detectable non-isotropic label, which is fluorescent molecule, chemiluminescent molecule, enzyme, cofactor, enzyme substrate or hapten. It hybridizes to the nucleic acid target region under moderate to highly stringent conditions to form a detectable target probe duplex. Preferred Method: The modifications are introduced by error-prone polymerase chain reaction (PCR), shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive, site-specific mutagenesis, gene reassembly and/or gene site saturated mutagenesis. The differences between the sequences are determined by identifying the polymorphisms.

USE - (I) is useful as encoding polypeptides having **esterase** activity. The polypeptide is an enzyme that catalyzes the hydrolysis of esters.

ADVANTAGE - The polypeptide has increased **esterase** activity and stability at increased pH temperature. It is stable to heat and is able to renature and regain activity after exposure to 60-105degreesC.

EXAMPLE - DNA encoding the enzymes of specified sequences above as well as specified deduced amino acid sequences, was initially amplified from a pBluescript vector containing the DNA by PCR technique. The restriction enzyme sites indicated parameters corresponding to the restriction enzyme sites on the bacterial expression. The pQE vector encoded antibiotic resistance, bacterial origin of replication, IPTG-regulatable promoter operator, ribosome binding site, 6His tag and restriction enzymes sites. Plasmid DNA was isolated and confirmed by restriction analysis. Clones containing the desired constructs were grown overnight in liquid culture. The cells were grown to an optical density of 0.4-0.6 Isopropyl-B-D thiogalacto pyranoside (IPTG) that was then added to the final concentration. The IPTG induced by inactivating the lad repressor, clearing the promoter operator leading to increased gene expression. Cells were grown an extra 3 to 4 hours. Cells were then harvested by centrifugation. (53 pages)

L37 ANSWER 2 OF 4 HCAPLUS COPYRIGHT 2003 ACS

AB The invention provides 3 human cyclic nucleotide-assocd. proteins (CNAP) and polynucleotides which identify and encode CNAP. CNAP-1 has chem. and structural similarity with Saccharomyces kluyveri adenylyl cyclase, CNAP-2 is similar to **Aquifex pyrophilus esterase** 28LC, and CNAP-3 is similar to human sol. guanylate cyclase large subunit. Protein motifs, tissue specificity, and disease assocn. of the 3 CNAP proteins are also provided. The invention also provides expression vectors, host cells, antibodies, and antagonists. The invention also provides methods for diagnosing, treating or preventing cell proliferative, autoimmune/inflammatory, neurol., vision, reproductive, and smooth muscle disorders.

L37 ANSWER 3 OF 4 MEDLINE

AB The recJ gene, identified in Escherichia coli, encodes a Mg(+2)-dependent 5'-to-3' exonuclease with high specificity for single-strand DNA. Genetic and biochemical experiments implicate RecJ exonuclease in homologous recombination, base excision, and methyl-directed mismatch repair. Genes encoding proteins with strong similarities to RecJ have been found in every eubacterial genome sequenced to date, with the exception of Mycoplasma and Mycobacterium tuberculosis. Multiple genes encoding proteins similar to RecJ are found in some eubacteria, including Bacillus and Helicobacter, and in the archaea. Among this divergent set of sequences, seven conserved motifs emerge. We demonstrate here that amino acids within six of these motifs are essential for both the biochemical and genetic functions of E. coli RecJ. These motifs may define interactions with Mg(2+) ions or substrate DNA. A large family of proteins more distantly related to RecJ is present in archaea, eubacteria, and eukaryotes, including a hypothetical protein in the MgPa adhesin operon of Mycoplasma, a domain of putative polyA polymerases in Synechocystis and **Aquifex**, PRUNE of Drosophila, and an exopolyphosphatase (PPX1) of Saccharomyces cereviseae. Because these six RecJ motifs are shared between exonucleases and exopolyphosphatases, they may constitute an ancient phosphoesterase domain now found in all kingdoms of life.

L37 ANSWER 4 OF 4 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI

AB A new DNA or RNA nucleic acid molecule encoding an enzyme (DNA sequence and protein sequence specified) can be contained on a vector and used to transform a host cell for production of the recombinant protein. The enzyme is preferably an **esterase**, able to transfer an amino group from an amino acid to an alpha-keto acid, and may be useful in e.g. cheese or paper manufacture or to study plant resistance to disease, etc. **Esterases** are used to convert esters to organic acids and alcohols. The claimed enzymes are thermostable and stable in organic solvents, so are well suited to industrial operations. The DNA is derived from Staphylococcus marinus F1-12LC, Pyrodictium sp. TAG17-17LC, Archaeoglobus venificus SNP6-24LC, Aquiflex **pyrophilus** 28LC and M11TL-29L, Thermococcus sp. CL-2-30LC, Aquiflex sp. VF5-34LC, Teredinibacter sp. 44L, Archaeoglobus fulgidus VC16-16MC and Sulfolobus solfataricus P1-8LC, prepared by amplification of genomic DNA using DNA primers (sequence specified). The nucleic acid encoding the **esterases** can be used as DNA probes or RNA probes to identify related sequences. (112pp)

```
=> s l24(8a)gene/q
FILE 'MEDLINE'
L38          30 L13(8A)GENE/Q

FILE 'SCISEARCH'
L39          35 L14(8A)GENE/Q

FILE 'LIFESCI'
L40          26 L15(8A)GENE/Q

FILE 'BIOTECHDS'
L41           9 L16(8A)GENE/Q

FILE 'BIOSIS'
L42          50 L17(8A)GENE/Q

FILE 'EMBASE'
L43          28 L18(8A)GENE/Q

FILE 'HCAPLUS'
L44          96 L19(8A)GENE/Q
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FILE 'NTIS'
L45          0 L20(8A)GENE/Q

FILE 'ESBIOBASE'
L46         27 L21(8A)GENE/Q

FILE 'BIOTECHNO'
L47         30 L22(8A)GENE/Q

FILE 'WPIDS'
L48          7 L23(8A)GENE/Q

TOTAL FOR ALL FILES
L49        338 L24(8A) GENE/Q

=> s l49 not 2002-2003/py
FILE 'MEDLINE'
        732373 2002-2003/PY
L50         25 L38 NOT 2002-2003/PY

FILE 'SCISEARCH'
       1279547 2002-2003/PY
L51         26 L39 NOT 2002-2003/PY

FILE 'LIFESCI'
        100291 2002-2003/PY
L52         21 L40 NOT 2002-2003/PY

FILE 'BIOTECHDS'
         27195 2002-2003/PY
L53          6 L41 NOT 2002-2003/PY

FILE 'BIOSIS'
        647654 2002-2003/PY
L54         35 L42 NOT 2002-2003/PY

FILE 'EMBASE'
        592164 2002-2003/PY
L55         20 L43 NOT 2002-2003/PY

FILE 'HCAPLUS'
       1444038 2002-2003/PY
L56         63 L44 NOT 2002-2003/PY

FILE 'NTIS'
         13299 2002-2003/PY
L57          0 L45 NOT 2002-2003/PY

FILE 'ESBIOBASE'
        377784 2002-2003/PY
L58         20 L46 NOT 2002-2003/PY

FILE 'BIOTECHNO'
        148719 2002-2003/PY
L59         22 L47 NOT 2002-2003/PY

FILE 'WPIDS'
       1410387 2002-2003/PY
L60          2 L48 NOT 2002-2003/PY

TOTAL FOR ALL FILES
L61        240 L49 NOT 2002-2003/PY
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=> dup rem l61
PROCESSING COMPLETED FOR L61
L62 74 DUP REM L61 (166 DUPLICATES REMOVED)

=> d tot

L62 ANSWER 1 OF 74 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
TI Thermostable DNA polymerase **gene** isolated from **aquifex pyrophilus** and its amino acid **sequence**;
enzyme gene production and mofidication from bacterium
AU CHOI J J; KWON S T
AN 2002-16315 BIOTECHDS
PI KR 2001113228 28 Dec 2001

L62 ANSWER 2 OF 74 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
TI **Aquifex pyrophilus** derived thermostable pyrophosphatase (ApyPpase) and coding **gene** used for genetic engineering and diagnosis of hereditary diseases;
vector plasmid pAPYP-mediated recombinant protein gene transfer and expression in Escherichia coli for use in disease diagnosis
AU HUH H S; KWON S T
AN 2002-14424 BIOTECHDS
PI KR 2001097348 8 Nov 2001

L62 ANSWER 3 OF 74 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
TI **Gene** encoding heat resistant alanine racemase of **Aquifex pyrophilus**, useful in medicine and food industry;
enzyme production, vector expression in bacterium, fermentation and incubation for food industry and medicine
AU YOO Y G
AN 2002-08972 BIOTECHDS
PI KR 2001083959 6 Sep 2001

L62 ANSWER 4 OF 74 MEDLINE DUPLICATE 2
TI Cytochromes c555 from the hyperthermophilic bacterium Aquifex aeolicus. 2. Heterologous production of soluble cytochrome c555s and investigation of the role of methionine residues.
SO BIOCHEMISTRY, (2001 Nov 13) 40 (45) 13690-8.
Journal code: 0370623. ISSN: 0006-2960.
AU Aubert C; Guerlesquin F; Bianco P; Leroy G; Tron P; Stetter K O; Bruschi M
AN 2001644001 MEDLINE

L62 ANSWER 5 OF 74 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 3
TI Cytochromes c555 from the hyperthermophilic bacterium Aquifex aeolicus (VF5). 1. Characterization of two highly homologous, soluble and membranous, cytochromes c555.
SO Biochemistry, (November 13, 2001) Vol. 40, No. 45, pp. 13681-13689. print.
ISSN: 0006-2960.
AU Baymann, Frauke; Tron, Pascale; Schoepp-Cothenet, Barbara (1); Aubert, Corinne; Bianco, Pierre; Stetter, Karl-Otto; Nitschke, Wolfgang; Schutz, Michael
AN 2001:567239 BIOSIS

L62 ANSWER 6 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Genes linked by fusion events are generally of the same functional category: a systematic analysis of 30 microbial genomes
SO Proceedings of the National Academy of Sciences of the United States of America (2001), 98(14), 7940-7945
CODEN: PNASA6; ISSN: 0027-8424
AU Yanai, Itai; Derti, Adnan; DeLisi, Charles
AN 2001:526462 HCAPLUS
DN 136:178666

L62 ANSWER 7 OF 74 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Differential effects of replacing Escherichia coli ribosomal protein L27 with its homologue from Aquifex aeolicus.
SO Journal of Bacteriology, (November, 2001) Vol. 183, No. 22, pp. 6565-6572. print.
ISSN: 0021-9193.
AU Maguire, Bruce A.; Manuilov, Anton V.; Zimmermann, Robert A. (1)
AN 2001:540050 BIOSIS

L62 ANSWER 8 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Comprehensive comparison between locations of orthologous genes on archaeal and bacterial genomes
SO Bioinformatics (2001), 17(9), 791-802
CODEN: BOINFP; ISSN: 1367-4803
AU Horimoto, Katsuhisa; Fukuchi, Satoshi; Mori, Kentaro
AN 2001:813196 HCAPLUS
DN 136:396906

L62 ANSWER 9 OF 74 MEDLINE DUPLICATE 4
TI Identification and cloning of partial mbh2 **gene** cluster of hyperthermophile **Aquifex pyrophilus**.
SO WEI SHENG WU HSUEH PAO [ACTA MICROBIOLOGICA SINICA], (2001 Dec) 41 (6) 674-9.
Journal code: 21610860R. ISSN: 0001-6209.
AU Lu J; Rakhely G; Kovacs K L; Xiao C; Zhou P
AN 2003044208 IN-PROCESS

L62 ANSWER 10 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Identification of novel essential Escherichia coli genes conserved among pathogenic bacteria
SO Journal of Molecular Microbiology and Biotechnology (2001), 3(3), 483-489
CODEN: JMMBFF; ISSN: 1464-1801
AU Freiberg, Christoph; Wieland, Bernd; Spaltmann, Frank; Ehlert, Kerstin; Brotz, Heike; Labischinski, Harald
AN 2001:348500 HCAPLUS
DN 135:104920

L62 ANSWER 11 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Phylogenetic analyses of two "archaeal" genes in Thermotoga maritima reveal multiple transfers between archaea and bacteria
SO Molecular Biology and Evolution (2001), 18(3), 362-375
CODEN: MBEVEO; ISSN: 0737-4038
AU Nesbo, Camilla L.; L'Haridon, Stephane; Stetter, Karl O.; Doolittle, W. Ford
AN 2001:186845 HCAPLUS
DN 135:283864

L62 ANSWER 12 OF 74 MEDLINE DUPLICATE 5
TI Prokaryotic structural maintenance of chromosomes (SMC) proteins: distribution, phylogeny, and comparison with MukBs and additional prokaryotic and eukaryotic coiled-coil proteins.
SO GENE, (2001 Oct 31) 278 (1-2) 253-64.
Journal code: 7706761. ISSN: 0378-1119.
AU Soppa J
AN 2001654625 MEDLINE

L62 ANSWER 13 OF 74 MEDLINE DUPLICATE 6
TI Expression in Escherichia coli of the thermostable inorganic pyrophosphatase from the Aquifex aeolicus and purification and characterization of the recombinant enzyme.
SO PROTEIN EXPRESSION AND PURIFICATION, (2001 Nov) 23 (2) 242-8.
Journal code: 9101496. ISSN: 1046-5928.
AU Hoe H S; Kim H K; Kwon S T

AN 2001642891 MEDLINE

L62 ANSWER 14 OF 74 MEDLINE DUPLICATE 7
TI Molecular cloning and characterization of thermostable DNA ligase from Aquifex pyrophilus, a hyperthermophilic bacterium.
SO EXTREMOPHILES, (2001 Jun) 5 (3) 161-8.
Journal code: 9706854. ISSN: 1431-0651.
AU Lim J H; Choi J; Han S J; Kim S H; Hwang H Z; Jin D K; Ahn B Y; Han Y S
AN 2002019598 MEDLINE

L62 ANSWER 15 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Genome of Aquifex aeolicus
SO Methods in Enzymology (2001), 330(Hyperthermophilic Enzymes, Part A), 158-169
CODEN: MENZAU; ISSN: 0076-6879
AU Swanson, Ronald V.
AN 2001:125818 HCAPLUS
DN 135:314007

L62 ANSWER 16 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Expression and characterization of the terminal heme synthetic enzymes from the hyperthermophile Aquifex aeolicus
SO FEMS Microbiology Letters (2001), 202(1), 115-119
CODEN: FMLED7; ISSN: 0378-1097
AU Wang, K.-F.; Dailey, T. A.; Dailey, H. A.
AN 2001:591698 HCAPLUS
DN 136:50095

L62 ANSWER 17 OF 74 MEDLINE DUPLICATE 8
TI Purification and properties of Aquifex aeolicus DNA polymerase expressed in Escherichia coli.
SO FEMS MICROBIOLOGY LETTERS, (2001 Jul 10) 201 (1) 73-7.
Journal code: 7705721. ISSN: 0378-1097.
AU Chang J R; Choi J J; Kim H K; Kwon S T
AN 2001390998 MEDLINE

L62 ANSWER 18 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Evolution of gene order conservation in prokaryotes
SO GenomeBiology [online computer file] (2001), 2(6), No pp. given
CODEN: GNBLFW; ISSN: 1465-6914
URL: http://genomebiology.com/2001/2/6/research/0020
AU Tamames, Javier
AN 2002:227287 HCAPLUS
DN 137:213424

L62 ANSWER 19 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Cloning and **sequence** of **Aquifex pyrophilus** superoxide dismutase **gene**, expression of the enzyme in Escherichia coli and its pharmaceutical applications
SO U.S., 17 pp.
CODEN: USXXAM
IN Han, Ye Sun; Yu, Yeon Gyu; Kim, Sung Hou; Lim, Jae Hwan; Ryu, Jae Ryeon; Choi, In Geol
AN 2000:157663 HCAPLUS
DN 132:204860

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 6033889	A	20000307	US 1998-8303	19980116

L62 ANSWER 20 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Cyclic glucan synthesis with thermostable branching enzyme for use in food production
SO Jpn. Kokai Tokkyo Koho, 12 pp.
CODEN: JKXXAF

IN Takada, Hiroki; Takabane, Takeshi; Kuriki, Takashi; Okada, Shigetaka
AN 2000:817136 HCAPLUS
DN 133:331188

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI JP 2000316581	A2	20001121	JP 1999-130833	19990512

L62 ANSWER 21 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Protein and cDNA sequences for a human ADP- ribosylglycohydrolase protein ARGHase, its expression and use
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 21 pp.
CODEN: CNXXEV
IN Li, Nenggan; Qian, Binzhi; Gao, Xin; Xiao, Huasheng; Chen, Zhu; Han, Zeguang
AN 2001:174517 HCAPLUS
DN 134:203430

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI CN 1264741	A	20000830	CN 2000-111778	20000302

L62 ANSWER 22 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Antibacterial agents that target lipid A biosynthesis in gram-negative bacteria: inhibition of diverse UDP-3-O-(R-3-hydroxymyristoyl)-N-acetylglucosamine deacetylases by substrate analogs containing zinc binding motifs
SO Journal of Biological Chemistry (2000), 275(15), 11002-11009
CODEN: JBCHA3; ISSN: 0021-9258
AU Jackman, Jane E.; Fierke, Carol A.; Tumey, L. Nathan; Pirrung, Michael; Uchiyama, Taketo; Tahir, S. Hasan; Hindsgaul, Ole; Raetz, Christian R. H.
AN 2000:270240 HCAPLUS
DN 133:27932

L62 ANSWER 23 OF 74 MEDLINE DUPLICATE 9
TI A soxA gene, encoding a diheme cytochrome c, and a sox locus, essential for sulfur oxidation in a new sulfur lithotrophic bacterium.
SO JOURNAL OF BACTERIOLOGY, (2000 Aug) 182 (15) 4278-87.
Journal code: 2985120R. ISSN: 0021-9193.
AU Mukhopadhyaya P N; Deb C; Lahiri C; Roy P
AN 2000396412 MEDLINE

L62 ANSWER 24 OF 74 MEDLINE DUPLICATE 10
TI Functionality of purified sigma(N) (sigma(54)) and a NifA-like protein from the hyperthermophile Aquifex aeolicus.
SO JOURNAL OF BACTERIOLOGY, (2000 Mar) 182 (6) 1616-23.
Journal code: 2985120R. ISSN: 0021-9193.
AU Studholme D J; Wigneshwererarai S R; Gallegos M T; Buck M
AN 2000158878 MEDLINE

L62 ANSWER 25 OF 74 MEDLINE DUPLICATE 11
TI Cloning and characterization of thermostable endoglucanase (Cel8Y) from the hyperthermophilic Aquifex aeolicus VF5.
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2000 Dec 20) 279 (2) 420-6.
Journal code: 0372516. ISSN: 0006-291X.
AU Kim J O; Park S R; Lim W J; Ryu S K; Kim M K; An C L; Cho S J; Park Y W; Kim J H; Yun H D
AN 2001111040 MEDLINE

L62 ANSWER 26 OF 74 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 12
TI Phylogenetic depth of the bacterial genera Aquifex and Thermotoga inferred from analysis of ribosomal protein, elongation factor, and RNA polymerase subunit sequences.
SO Journal of Molecular Evolution, (April, 2000) Vol. 50, No. 4, pp. 366-380.

ISSN: 0022-2844.
AU Bocchetta, Maurizio; Gribaldo, Simonetta; Sanangelantoni, Annamaria; Cammarano, Piero (1)
AN 2000:241251 BIOSIS

L62 ANSWER 27 OF 74 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Hyperthemostable AONS: The first committed enzyme in E. coli biotin biosynthesis has a tropical relative.
SO Biochemical Society Transactions, (October, 2000) Vol. 28, No. 5, pp. A316. print.
Meeting Info.: 18th International Congress of Biochemistry and Molecular Biology Birmingham, UK July 16-20, 2000
ISSN: 0300-5127.
AU Mullan, Lisa J. (1); Webster, Scott P. (1); Alexeev, Dmitriy G. (1); Baxter, Robert L. (1)
AN 2001:102325 BIOSIS

L62 ANSWER 28 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Polypurine.polypyrimidine sequences in complete bacterial genomes: preference for polypurines in protein-coding regions
SO Gene (2000), 242(1-2), 275-283
CODEN: GENED6; ISSN: 0378-1119
AU Raghavan, Sowmya; Hariharan, Ramesh; Brahmachari, Samir K.
AN 2000:154073 HCAPLUS
DN 132:304159

L62 ANSWER 29 OF 74 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Extremely thermostable elongation factor G from Aquifex aeolicus: Cloning, expression, purification, and characterization in a heterologous translation system.
SO Protein Expression and Purification, (April, 2000) Vol. 18, No. 3, pp. 257-261.
ISSN: 1046-5928.
AU Martemyanov, Kirill A.; Liljas, Anders; Gudkov, Anatoly T. (1)
AN 2000:233620 BIOSIS

L62 ANSWER 30 OF 74 LIFESCI COPYRIGHT 2003 CSA DUPLICATE 13
TI Reverse gyrase from hyperthermophiles: Probable transfer of a thermoadaptation trait from Archaea to Bacteria
SO Trends in Genetics [Trends Genet.], (20000400) vol. 16, no. 4, pp. 152-156.
ISSN: 0168-9525.
AU Forterre, P.; De La Tour, C.B.; Philippe, H.; Duguet, M.
AN 2000:76087 LIFESCI

L62 ANSWER 31 OF 74 MEDLINE DUPLICATE 14
TI The alternative sigma factor sigma(28) of the extreme thermophile Aquifex aeolicus restores motility to an Escherichia coli fliA mutant.
SO FEMS MICROBIOLOGY LETTERS, (2000 Oct 1) 191 (1) 103-7.
Journal code: 7705721. ISSN: 0378-1097.
AU Studholme D J; Buck M
AN 2001045810 MEDLINE

L62 ANSWER 32 OF 74 SCISEARCH COPYRIGHT 2003 THOMSON ISIDUPLICATE 15
TI Characterization of a solvent resistant and thermostable aminopeptidase from the hyperthermophillic bacterium, Aquifex aeolicus
SO ENZYME AND MICROBIAL TECHNOLOGY, (JUL 2000) Vol. 27, No. 1-2, pp. 83-88.
Publisher: ELSEVIER SCIENCE INC, 655 AVENUE OF THE AMERICAS, NEW YORK, NY 10010.
ISSN: 0141-0229.
AU Khan A R; Nirasawa S; Kaneko S; Shimonishi T; Hayashi K (Reprint)
AN 2000:506413 SCISEARCH

L62 ANSWER 33 OF 74 SCISEARCH COPYRIGHT 2003 THOMSON ISIDUPLICATE 16

TI Molecular cloning of an extremely thermostable alanine racemase from Aquifex pyrophilus and enzymatic characterization of the expressed protein
SO JOURNAL OF BIOCHEMISTRY AND MOLECULAR BIOLOGY, (31 JAN 2000) Vol. 33, No. 1, pp. 82-88.
Publisher: SPRINGER-VERLAG SINGAPORE PTE LTD, #04-01 CENCON I, 1 TANNERY RD, SINGAPORE 347719, SINGAPORE.
ISSN: 1225-8687.
AU Kim S S; Yu Y G (Reprint)
AN 2000:90575 SCISEARCH

L62 ANSWER 34 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Genome evolution. Gene fusion versus gene fission
SO Trends in Genetics (2000), 16(1), 9-11
CODEN: TRGEE2; ISSN: 0168-9525
AU Snel, Berend; Bork, Peer; Huynen, Martijn
AN 2000:55022 HCAPLUS
DN 132:190460

L62 ANSWER 35 OF 74 MEDLINE DUPLICATE 17
TI The biology of enhancer-dependent transcriptional regulation in bacteria: insights from genome sequences.
SO FEMS MICROBIOLOGY LETTERS, (2000 May 1) 186 (1) 1-9. Ref: 25
Journal code: 7705721. ISSN: 0378-1097.
AU Studholme D J; Buck M
AN 2000395687 MEDLINE

L62 ANSWER 36 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Interkingdom gene fusions
SO GenomeBiology [online computer file] (2000), 1(6), No pp. given
CODEN: GNBLFW; ISSN: 1465-6914
URL: http://www.genomebiology.com/retriever.asp?url=/2000/1/6/research/0013
AU Wolf, Yuri I.; Kondrashov, Alexey S.; Koonin, Eugene V.
AN 2001:182692 HCAPLUS
DN 136:15880

L62 ANSWER 37 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Sequences of members of the novel bacterial yihA gene family, and uses thereof in screening for novel broad spectrum antibiotics
SO PCT Int. Appl., 42 pp.
CODEN: PIXXD2
IN Arigoni, Fabrizio; Edgerton, Michael David; Loferer, Hannes; Peitsch, Manuel C.
AN 1999:691219 HCAPLUS
DN 131:333017

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9954474	A2	19991028	WO 1999-EP2640	19990420
WO 9954474	A3	20000504		
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9937090	A1	19991108	AU 1999-37090	19990420

L62 ANSWER 38 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Sequences of members of the novel bacterial ycfB gene family, and uses thereof in screening for novel broad spectrum antibiotics
SO PCT Int. Appl., 56 pp.

CODEN: PIXXD2
IN Arigoni, Fabrizio; Edgerton, Michael David; Loferer, Hannes; Peitsch, Manuel C.
AN 1999:691207 HCAPLUS
DN 131:333015

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9954462	A2	19991028	WO 1999-EP2638	19990420
WO 9954462	A3	20000622		

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AU 9937089	A1	19991108	AU 1999-37089	19990420

L62 ANSWER 39 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Gene and amino acid sequences of DNA polymerase III holoenzyme subunits from Thermus thermophilus
SO PCT Int. Appl., 212 pp.
CODEN: PIXXD2
IN McHenry, Charles S.; Seville, Mark; Cull, Millard G.; Chen, Joe Yu; Kery, Vladimir
AN 1999:194247 HCAPLUS
DN 130:248757

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9913060	A1	19990318	WO 1998-US18946	19980911

W: AU, CA, JP, MX
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

US 6238905	B1	20010529	US 1997-928213	19970912
CA 2303400	AA	19990318	CA 1998-2303400	19980911
AU 9892296	A1	19990329	AU 1998-92296	19980911
EP 1012248	A1	20000628	EP 1998-944849	19980911

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI

L62 ANSWER 40 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Preparation of 6-O-substituted ketolide glycosides as antibacterial agents
SO Eur. Pat. Appl., 18 pp.
CODEN: EPXXDW
IN Chartreaux, Fabienne; Klich, Michel; Schio, Laurent
AN 1999:96038 HCAPLUS
DN 130:125344

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI EP 894805	A1	19990203	EP 1998-401840	19980721

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

FR 2766488	A1	19990129	FR 1997-9352	19970723
FR 2766488	B1	20000218		
US 5968939	A	19991019	US 1998-120642	19980722
JP 11092493	A2	19990406	JP 1998-207950	19980723

L62 ANSWER 41 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Structure-specific tRNA-binding protein from the extreme thermophile Aquifex aeolicus
SO EMBO Journal (1999), 18(12), 3475-3483
CODEN: EMJODG; ISSN: 0261-4189

AU Morales, Arturo J.; Swairjo, Manal A.; Schimmel, Paul
AN 1999:433529 HCAPLUS
DN 131:196766

L62 ANSWER 42 OF 74 MEDLINE DUPLICATE 18
TI Sequences and evolutionary analyses of eukaryotic-type protein kinases from Streptomyces coelicolor A3(2).
SO MICROBIOLOGY, (1999 Dec) 145 (Pt 12) 3343-52.
Journal code: 9430468. ISSN: 1350-0872.
AU Ogawara H; Aoyagi N; Watanabe M; Urabe H
AN 2000090459 MEDLINE

L62 ANSWER 43 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Conservation of xer site-specific recombination genes in bacteria
SO Molecular Microbiology (1999), 34(5), 1146-1148
CODEN: MOMIEE; ISSN: 0950-382X
AU Recchia, Gavin D.; Sherratt, David J.
AN 2000:26678 HCAPLUS
DN 132:176460

L62 ANSWER 44 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Evolutionary relationships among photosynthetic prokaryotes (Heliobacterium chlorum, Chloroflexus aurantiacus, cyanobacteria, Chlorobium tepidum and proteobacteria): implications regarding the origin of photosynthesis
SO Molecular Microbiology (1999), 32(5), 893-906
CODEN: MOMIEE; ISSN: 0950-382X
AU Gupta, Radhey S.; Mukhtar, Tariq; Singh, Bhag
AN 1999:380511 HCAPLUS
DN 131:182139

L62 ANSWER 45 OF 74 MEDLINE DUPLICATE 19
TI A [2Fe-2S] protein from the hyperthermophilic bacterium Aquifex aeolicus.
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1999 Aug 11) 261 (3) 885-9.
Journal code: 0372516. ISSN: 0006-291X.
AU Chatelet C; Gaillard J; Petillot Y; Louwagie M; Meyer J
AN 1999373173 MEDLINE

L62 ANSWER 46 OF 74 MEDLINE DUPLICATE 20
TI Extremely thermostable serine-type protease from Aquifex pyrophilus. Molecular cloning, expression, and characterization.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 Jan 8) 274 (2) 881-8.
Journal code: 2985121R. ISSN: 0021-9258.
AU Choi I G; Bang W G; Kim S H; Yu Y G
AN 1999091626 MEDLINE

L62 ANSWER 47 OF 74 MEDLINE DUPLICATE 21
TI A new member of the endonuclease III family of DNA repair enzymes that removes methylated purines from DNA.
SO CURRENT BIOLOGY, (1999 Jun 17) 9 (12) 653-6.
Journal code: 9107782. ISSN: 0960-9822.
AU Begley T J; Haas B J; Noel J; Shekhtman A; Williams W A; Cunningham R P
AN 1999307502 MEDLINE

L62 ANSWER 48 OF 74 MEDLINE DUPLICATE 22
TI RNA polymerase of Aquifex pyrophilus: implications for the evolution of the bacterial rpoBC operon and extremely thermophilic bacteria.
SO JOURNAL OF MOLECULAR EVOLUTION, (1999 May) 48 (5) 528-41.
Journal code: 0360051. ISSN: 0022-2844.
AU Klenk H P; Meier T D; Durovic P; Schwass V; Lottspeich F; Dennis P P; Zillig W
AN 1999214260 MEDLINE

L62 ANSWER 49 OF 74 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 23
TI Discontinuous occurrence of the hsp70 (dnaK) gene among Archaea and sequence features of HSP70 suggest a novel outlook on phylogenies inferred from this protein.
SO Journal of Bacteriology, (Jan., 1999) Vol. 181, No. 2, pp. 434-443. ISSN: 0021-9193.
AU Gribaldo, Simonetta; Lumia, Valentina; Creti, Roberta; Conway De Macario, Everly; Sanangelantoni, Annamaria; Cammarano, Piero (1)
AN 1999:98324 BIOSIS

L62 ANSWER 50 OF 74 MEDLINE DUPLICATE 24
TI Functional and biochemical characterization of a recombinant 3-Deoxy-D-manno-octulosonic acid 8-phosphate synthase from the hyperthermophilic bacterium Aquifex aeolicus.
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1999 Sep 24) 263 (2) 346-51.
Journal code: 0372516. ISSN: 0006-291X.
AU Duewel H S; Sheflyan G Y; Woodard R W
AN 1999423466 MEDLINE

L62 ANSWER 51 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Distribution of species specific gene family in microorganisms
SO Genome Informatics Series (1999), 10, 326-327
CODEN: GINSE9; ISSN: 0919-9454
AU Ara, Takeshi; Suzuki, Kenji; Matuda, Hideo; Mori, Hirotada
AN 2000:80333 HCAPLUS
DN 133:84950

L62 ANSWER 52 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Archaeal and bacterial hyperthermophiles: horizontal gene exchange or common ancestry? Comments
SO Trends in Genetics (1999), 15(8), 298-299
CODEN: TRGEE2; ISSN: 0168-9525
AU Kyrpides, Nikos C.; Olsen, Gary J.
AN 1999:503535 HCAPLUS
DN 131:269434

L62 ANSWER 53 OF 74 MEDLINE DUPLICATE 25
TI Molecular cloning, expression, and characterization of a thermostable glutamate racemase from a hyperthermophilic bacterium, Aquifex pyrophilus.
SO EXTREMOPHILES, (1999 Aug) 3 (3) 175-83.
Journal code: 9706854. ISSN: 1431-0651.
AU Kim S S; Choi I G; Kim S H; Yu Y G
AN 1999411974 MEDLINE

L62 ANSWER 54 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Studies of codon usage and tRNA genes of 18 unicellular organisms and quantification of Bacillus subtilis tRNAs: gene expression level and species-specific diversity of codon usage based on multivariate analysis
SO Gene (1999), 238(1), 143-155
CODEN: GENED6; ISSN: 0378-1119
AU Kanaya, Shigehiko; Yamada, Yuko; Kudo, Yoshihiro; Ikemura, Toshimichi
AN 1999:716490 HCAPLUS
DN 132:19581

L62 ANSWER 55 OF 74 SCISEARCH COPYRIGHT 2003 THOMSON ISIDUPLICATE 26
TI A sequencer of thirty bases that is highly repetitive in archaebacterial genomes
SO PROCEEDINGS OF THE JAPAN ACADEMY SERIES B-PHYSICAL AND BIOLOGICAL SCIENCES, (JAN 1999) Vol. 75, No. 1, pp. 16-21.
Publisher: JAPAN ACAD, 7-32 UENO PARK, TOKYO 110, JAPAN.
ISSN: 0386-2208.
AU Suckow J M; Suzuki M (Reprint)

AN 1999:169952 SCISEARCH

L62 ANSWER 56 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Thermostable mutL genes and proteins and their uses in nucleic acid amplification and hybridization
SO PCT Int. Appl., 148 pp.
CODEN: PIXXD2
IN Wetmur, James G.
AN 1998:65999 HCAPLUS
DN 128:150360

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9801562	A1	19980115	WO 1997-US11567	19970701
W: AU, CA, IL, JP				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6294325	B1	20010925	US 1996-676444	19960705
AU 9736486	A1	19980202	AU 1997-36486	19970701

L62 ANSWER 57 OF 74 WPIDS (C) 2003 THOMSON DERWENT
TI Novel Aquifex pyrophilus superoxide dismutase polynucleotides and polypeptides, used for the treatment of inflammation, autoimmune disorders, and chromosome lesions.

PI KR 98065913	A	19981015 (199950)*	1p	C12N015-53
US 6033889	A	20000307 (200022)B	17p	C12N009-02
KR 183362	B1	19990401 (200113)		C12N015-53

IN CHOE, I; HAN, Y; LIM, J; RYU, J; YOO, Y; CHOI, I G; HAN, Y S; KIM, S H; LIM, J H; RYOO, J R; YOO, Y G; RYU, J R; YU, Y G

L62 ANSWER 58 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Aquifex pyrophilus
SO Bacterial Genomes (1998), 605-607. Editor(s): De Bruijn, Frans J.; Lupski, James R.; Weinstock, George M. Publisher: Chapman & Hall, New York, N. Y.
CODEN: 65KVAK
AU Schmitt, Rudiger
AN 1997:778269 HCAPLUS
DN 128:84986

L62 ANSWER 59 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI The complete genome of the hyperthermophilic bacterium Aquifex aeolicus
SO Nature (London) (1998), 392(6674), 353-358
CODEN: NATUAS; ISSN: 0028-0836
AU Deckert, Gerard; Warren, Patrick V.; Gaasterland, Terry; Young, William G.; Lenox, Anna L.; Graham, David E.; Overbeek, Ross; Snead, Marjory A.; Keller, Martin; Aujay, Monette; Huber, Robert; Feldman, Robert A.; Short, Jay M.; Olsen, Gary J.; Swanson, Ronald V.
AN 1998:229920 HCAPLUS
DN 128:253667

L62 ANSWER 60 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Sequence and phylogenetic position of a class II aldolase gene in the amitochondriate protist, Giardia lamblia
SO Gene (1998), 222(2), 163-168
CODEN: GENED6; ISSN: 0378-1119
AU Henze, Katrin; Morrison, Hilary G.; Sogin, Mitchell L.; Muller, Miklos
AN 1998:809228 HCAPLUS
DN 130:163804

L62 ANSWER 61 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Genomic analysis of the genes encoding ribosomal proteins in eight eubacterial species and Saccharomyces cerevisiae
SO Genome Informatics Series (1998), 9, 3-12
CODEN: GINSE9; ISSN: 0919-9454
AU Fujita, Katsutoshi; Baba, Tomoya; Isono, Katsumi

AN 1999:175410 HCAPLUS
DN 131:68899

L62 ANSWER 62 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Novel bacterial esterases identification after recombinant expression and esterase and cDNA sequences
SO PCT Int. Appl., 112 pp.
CODEN: PIXXD2
IN Robertson, Dan E.; Murphy, Dennis; Reid, John; Maffia, Anthony M.; Link, Steven; Swanson, Ronald V.; Warren, Patrick V.; Kosmotka, Anna; Callen, Walter
AN 1997:568292 HCAPLUS
DN 127:231209

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9730160	A1	19970821	WO 1997-US2039	19970211
	W: AU, CA, IL, JP, US				
	RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 5942430	A	19990824	US 1996-602359	19960216
	CA 2246737	AA	19970821	CA 1997-2246737	19970211
	AU 9721195	A1	19970902	AU 1997-21195	19970211
	AU 716692	B2	20000302		
	EP 880590	A1	19981202	EP 1997-906528	19970211
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 2001505403	T2	20010424	JP 1997-529411	19970211

L62 ANSWER 63 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Thermostable transaminase- and aminotransferase-encoding DNA sequences for industrial uses such as catalyzing amino acid reactions with .alpha.-keto acids
SO PCT Int. Appl., 94 pp.
CODEN: PIXXD2
IN Warren, Patrick V.; Swanson, Ronald V.
AN 1997:542516 HCAPLUS
DN 127:217041

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9729187	A1	19970814	WO 1997-US1094	19970121
	W: AU, CA, IL, JP, US				
	RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 5814473	A	19980929	US 1996-599171	19960209
	US 5962283	A	19991005	US 1996-646590	19960508
	AU 9718367	A1	19970828	AU 1997-18367	19970121
	AU 718147	B2	20000406		
	JP 2000505291	T2	20000509	JP 1997-528527	19970121
	EP 1015563	A1	20000705	EP 1997-903936	19970121
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

L62 ANSWER 64 OF 74 MEDLINE DUPLICATE 27
TI Cloning and expression of superoxide dismutase from Aquifex pyrophilus, a hyperthermophilic bacterium.
SO FEBS LETTERS, (1997 Apr 7) 406 (1-2) 142-6.
Journal code: 0155157. ISSN: 0014-5793.
AU Lim J H; Yu Y G; Choi I G; Ryu J R; Ahn B Y; Kim S H; Han Y S
AN 97263490 MEDLINE

L62 ANSWER 65 OF 74 MEDLINE DUPLICATE 28
TI Random **sequence** analysis of genomic DNA of a hyperthermophile: **Aquifex pyrophilus**.
SO EXTREMOPHILES, (1997 Aug) 1 (3) 125-34.
Journal code: 9706854. ISSN: 1431-0651.
AU Choi I G; Kim S S; Ryu J R; Han Y S; Bang W G; Kim S H; Yu Y G

AN 1998343912 MEDLINE

L62 ANSWER 66 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Cloning and expression of thermostable mutS genes and proteins from hyperthermophilic bacteria and their applications to improve fidelity in DNA amplification techniques
SO PCT Int. Appl., 92 pp.
CODEN: PIXXD2
IN Wetmur, James G.
AN 1997:85214 HCAPLUS
DN 126:85652

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9639525	A1	19961212	WO 1996-US8677	19960604
W: CA, IL, JP				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 5877280	A	19990302	US 1995-468558	19950606
CA 2221451	AA	19961212	CA 1996-2221451	19960604
EP 832240	A1	19980401	EP 1996-919058	19960604
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 11511010	T2	19990928	JP 1996-501189	19960604

L62 ANSWER 67 OF 74 MEDLINE DUPLICATE 29
TI Sensitivity of ribosomes of the hyperthermophilic bacterium Aquifex pyrophilus to aminoglycoside antibiotics.
SO JOURNAL OF BACTERIOLOGY, (1996 Mar) 178 (6) 1762-5.
Journal code: 2985120R. ISSN: 0021-9193.
AU Bocchetta M; Huber R; Cammarano P
AN 96198182 MEDLINE

L62 ANSWER 68 OF 74 MEDLINE DUPLICATE 30
TI Flagellar structure and hyperthermophily: analysis of a single flagellin **gene** and its product in **Aquifex pyrophilus**.
SO JOURNAL OF BACTERIOLOGY, (1995 Nov) 177 (22) 6630-7.
Journal code: 2985120R. ISSN: 0021-9193.
AU Behammer W; Shao Z; Mages W; Rachel R; Stetter K O; Schmitt R
AN 96062250 MEDLINE

L62 ANSWER 69 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Root of the universal tree of life based on ancient aminoacyl-tRNA synthetase gene duplications
SO Proceedings of the National Academy of Sciences of the United States of America (1995), 92(7), 2441-5
CODEN: PNASA6; ISSN: 0027-8424
AU Brown, James R.; Doolittle, W. Ford
AN 1995:479772 HCAPLUS
DN 123:191805

L62 ANSWER 70 OF 74 MEDLINE DUPLICATE 31
TI Arrangement and nucleotide sequence of the gene (fus) encoding elongation factor G (EF-G) from the hyperthermophilic bacterium Aquifex pyrophilus: phylogenetic depth of hyperthermophilic bacteria inferred from analysis of the EF-G/fus sequences.
SO JOURNAL OF MOLECULAR EVOLUTION, (1995 Dec) 41 (6) 803-12.
Journal code: 0360051. ISSN: 0022-2844.
AU Bocchetta M; Ceccarelli E; Creti R; Sanangelantoni A M; Tiboni O; Cammarano P
AN 96139013 MEDLINE

L62 ANSWER 71 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI Cloning, sequencing, and expression of RecA proteins from three distantly related thermophilic eubacteria
SO Journal of Biological Chemistry (1994), 269(41), 25928-35

CODEN: JBCHA3; ISSN: 0021-9258
AU Wetmur, James G.; Wong, Daphne M.; Ortiz, Benjamin; Tong, Jie; Reichert, Frederick; Gelfand, David H.
AN 1994:624939 HCAPLUS
DN 121:224939

L62 ANSWER 72 OF 74 HCAPLUS COPYRIGHT 2003 ACS
TI A physical map of the hyperthermophilic bacterium Aquifex pyrophilus chromosome
SO Journal of Bacteriology (1994), 176(21), 6776-80
CODEN: JOBAAY; ISSN: 0021-9193
AU Shao, Zhixin; Mages, Wolfgang; Schmitt, Ruediger
AN 1994:694242 HCAPLUS
DN 121:294242

L62 ANSWER 73 OF 74 MEDLINE DUPLICATE 32
TI Phylogenetic analysis of the hyperthermophilic pink filament community in Octopus Spring, Yellowstone National Park.
SO APPLIED AND ENVIRONMENTAL MICROBIOLOGY, (1994 Jun) 60 (6) 2113-9.
Journal code: 7605801. ISSN: 0099-2240.
AU Reysenbach A L; Wickham G S; Pace N R
AN 94304181 MEDLINE

L62 ANSWER 74 OF 74 MEDLINE DUPLICATE 33
TI A phylogenetic analysis of Aquifex pyrophilus.
SO SYSTEMATIC AND APPLIED MICROBIOLOGY, (1992 Aug) 15 (3) 352-6.
Journal code: 8306133. ISSN: 0723-2020.
(Investigators: Woese C R, U IL, Urbana, Dept Microbiology) Report No.: NASA-00016510.
AU Burggraf S; Olsen G J; Stetter K O; Woese C R
AN 2001658644 MEDLINE

=> d ab 66-
YOU HAVE REQUESTED DATA FROM 9 ANSWERS - CONTINUE? Y/(N):y

L62 ANSWER 66 OF 74 HCAPLUS COPYRIGHT 2003 ACS
AB Isolated nucleic acids are provided which encode a thermostable protein which binds specifically to bulge loops in a heteroduplex nucleic acid and recombinant vectors comprising nucleic acid which encodes a thermostable protein which binds specifically to bulge loops in a heteroduplex nucleic acid. MutS genes were cloned into Escherichia coli from 2 distantly related hyperthermophilic eubacteria, Aquifex pyrophilus and Thermotoga maritima, based on PCR technol. without the need for library construction. Based on the binding activity for bulge loops in a heteroduplex, the recombinant MutS proteins can reduce DNA misincorporation in an amplification reaction, and thus be used in methods for detecting a nucleic acid which includes a specific sequence, amplifying a nucleic acid comprising a specific sequence, and selecting against a nucleic acid comprising a specific sequence. Allele-specific amplification with matched primers demonstrates that MutS binding to a variety of mismatched primer-template complexes inhibits initiation of polymn. With mismatched internal oligonucleotide, propagation of polymn. can be inhibited by forming a MutS-internal duplex mismatch complex; MutS-mediated selective amplification occurs at each PCR cycle, if needed.

L62 ANSWER 67 OF 74 MEDLINE DUPLICATE 29
AB A poly(U)-programmed cell-free system from the hyperthermophilic bacterium Aquifex pyrophilus has been developed, and the susceptibility of Aquifex ribosomes to the miscoding-inducing and inhibitory actions of all known classes of aminoglycoside antibiotics has been assayed at temperatures (75 to 80 degrees C) close to the physiological optimum for cell growth. Unlike Thermotoga maritima ribosomes, which are systematically refractory to all known classes of aminoglycoside compounds (P. Londei, S.

Altamura, R. Huber, K. O. Stetter, and P. Cammarano, J. offteriol. 170-4353-4360, 1988), Aquifex ribosomes are susceptible to all of the aminoglycosides tested (disubstituted 2-deoxystreptamines, monosubstituted 2-deoxystreptamines, sand streptidine compounds). The significance of this result in light of the **Aquifex** and Thermotoga placements in phylogenetic trees of molecular **sequences** is discussed.

L62 ANSWER 68 OF 74 MEDLINE DUPLICATE 30
AB The polytrichously inserted flagella of Aquifex pyrophilus, a marine hyperthermophilic bacterium growing at 85 degrees C, were isolated and purified. Electron micrographs of the 19-nm-diameter flagellar filaments show prominent helical arrays of subunits. The primary structure of these 54-kDa flagellin monomers determining the helical shape and heat stability of filaments was of particular interest. The genomic region encoding the flagellin subunit (flaA gene) and an upstream open reading frame (orf1) were cloned and sequenced. The 1,503-bp flaA and 696-bp orf1 are preceded by separate sigma 28-like promoters and ribosome-binding motifs and succeeded by palindromic transcription terminators. Both genes are actively transcribed, but the nature and function of the orf1-encoded 231-residue polypeptide remain unknown. The deduced primary structure of the 501-amino-acid flagellin encoded by flaA consists of conserved N- and C-terminal regions and a variable 246-residue central domain. In comparison to mesophilic flagellins, the thermostable A. pyrophilus flagellin is characterized by increases in aromatic residues and prolines as well as by a 7.9% +/- 3.2% increase in all hydrophobic residues that is balanced by a respective decrease in hydrophilic residues. This composition is thought to form more compact flagellin monomers and stable interface contacts between neighboring subunits in the polymer.

L62 ANSWER 69 OF 74 HCAPLUS COPYRIGHT 2003 ACS
AB Universal trees based on sequences of single gene homologs cannot be rooted. Iwabe et al. [Iwabe, N., Kuman, K.-I., Hasegawa, M., Osawa, S. and Miyata, T. (1989) Proc. Natl. Acad. Sci. USA 86, 9355-9359] circumvented this problem by using ancient gene duplications that predated the last common ancestor of all living things. Their sep., reciprocally rooted gene trees for elongation factors and ATPase subunits showed Bacteria (eubaceria) as branching first from the universal tree with Archea (archaebacteria) and Eucarya (eukaryotes) as sister groups. Given its topical importance to evolutionary biol. and concerns about the appropriateness of the ATPase data set, an evaluation of the universal tree root using other ancient gene duplications is essential. In this study, we derive a rooting for the universal tree using aminoacyl-tRNA synthetase genes, an extensive multigene family whose divergence likely preceded that of prokaryotes and eukaryotes. An approx. 1600-bp conserved region was sequenced from the isoleucyl-tRNA synthetases of several species representing deep evolutionary branches of eukaryotes (Nosema locustae), Bacteria (Aquifex pyrophilus and Thermotoga maritima) and Archea (Pyrococcus furiosus and Sulfolobus acidocaldarius). In addn., a new valyl-tRNA synthetase was characterized from the protist Trichomonas vaginalis. Different phylogenetic methods were used to generate trees of isoleucyl-tRNA synthetases rooted by valyl- and leucyl-tRNA synthetases. All isoleucyl-tRNA synthetase trees showed Archaea and Eucarya as sister groups, providing strong confirmation for the universal tree rooting reported by Iwabe et al. As well, there was strong support for the monopoly (sensu Hennig) of Archea. The valyl-tRNA synthetase gene from Tr. vaginalis clustered with other eukaryotic VaIRS genes, which may have been transferred from the mitochondrial genome to the nuclear genome, suggesting that this amitochondrial trichomonad once harbored and endosymbiotic bacterium.

L62 ANSWER 70 OF 74 MEDLINE DUPLICATE 31
AB The **gene** fus (for EF-G) of the hyperthermophilic bacterium **Aquifex pyrophilus** was cloned and **sequenced**.
Unlike the other bacteria, which display the streptomycin-operon

arrangement of EF **genes** (5'-rps12-rps7-fus-tuf-3'), the **Aquifex** fus **gene** (700 codons) is not preceded by the two small ribosomal subunit genes although it is still followed by a tuf gene (for EF-Tu). The opposite strand upstream from the EF-G coding locus revealed an open reading frame (ORF) encoding a polypeptide having 52.5% identity with an E. coli protein (the pdxJ gene product) involved in pyridoxine condensation. The Aquifex EF-G was aligned with available homologs representative of Deinococci, high G+C Gram positives, Proteobacteria, cyanobacteria, and several Archaea. Outgroup-rooted phylogenies were constructed from both the amino acid and the DNA sequences using first and second codon positions in the alignments except sites containing synonymous changes. Both datasets and alternative tree-making methods gave a consistent topology, with Aquifex and Thermotoga maritima (a hyperthermophile) as the first and the second deepest offshoots, respectively. However, the robustness of the inferred phylogenies is not impressive. The branching of Aquifex more deeply than Thermotoga and the branching of Thermotoga more deeply than the other taxa examined are given at bootstrap values between 65 and 70% in the fus-based phylogenies, while the EF-G(2)-based phylogenies do not provide a statistically significant level of support (< or = 50% bootstrap confirmation) for the emergence of Thermotoga between Aquifex and the successive offshoot (Thermus genus). At present, therefore, the placement of Aquifex at the root of the bacterial tree, albeit reproducible, can be asserted only with reservation, while the emergence of Thermotoga between the Aquificales and the Deinococci remains (statistically) indeterminate.

L62 ANSWER 71 OF 74 HCAPLUS COPYRIGHT 2003 ACS
AB Sequences of the recA genes of the highly divergent thermophilic eubacteria Thermus aquaticus (and Thermus thermophilus), Thermotoga maritima, and Aquifex pyrophilus were detd. from fragments derived by polymerase chain reaction (PCR) with degenerate primers and from inverse PCR products obtained using unique primers based on the fragment sequences. The source of the PCR products was verified by Southern hybridization. Complete PCR-derived recA genes were cloned into an expression vector regulated by a temp.-sensitive .lambda.-repressor, and independently derived clones expressing thermostable RecA were selected. DNA sequences were verified to be authentic by direct cycle-sequencing of PCR products and/or sequencing of several clones. In contrast to Escherichia coli RecA protein, all the purified thermophilic RecA proteins exhibited single-stranded DNA-dependent ATPase activity optima above 70 .degree.C. Phylogenetic anal. of RecA sequences suggested that the thermophilic RecA proteins were at least as different from one another as were Gram-pos. organisms, mesophilic Gram-neg. organisms, and cyanobacteria. In spite of substantial sequence divergence, interesting characteristics of the thermostable RecA proteins included increased valine content, common amino acid replacements at two highly conserved sites, and an increase in the calcd. isoelec. point of approx. a full pH unit.

L62 ANSWER 72 OF 74 HCAPLUS COPYRIGHT 2003 ACS
AB A genomic map of the hyperthermophilic hydrogen-oxidizing bacterium Aquifex pyrophilus was established with NotI (GC/GGCCGC), SpeI (A/CTAGT), and XbaI (T/CTAGA). Linking clones and cross-hybridization of restriction fragments revealed a single circular chromosome of 1.6 Mbp. A single flagellin gene and six rRNA gene units were located on this map by Southern hybridization.

L62 ANSWER 73 OF 74 MEDLINE DUPLICATE 32
AB The phylogenetic diversity of a well-known pink filament community associated with the 84 to 88 degrees C outflow from Octopus Spring, Yellowstone National Park, was examined. Three phylogenetic types ("phylotypes"), designated EM 3, EM 17, and EM 19, were identified by cloning and sequencing the small subunit rRNA genes (16S rDNA) obtained by PCR amplification of mixed-population DNA. All three phylotypes diverge

deeply within the phylogenetic domain Bacteria sensu Woese (C. R. Woese, O. Kandler, and M. L. Wheelis, Proc. Natl. Acad. Sci. USA 87:4576-4579, 1990). No members of the Archaea or Eucarya were detected. EM 3 comprises a unique lineage within the Thermotogales group, and EM 17 and EM 19 are affiliated with the Aquificales. A total of 35 clones were examined, of which the majority (26 clones) were of a single **sequence** type (EM 17) closely related to **Aquifex pyrophilus**. In situ hybridization with clone-specific probes attributes the majority sequence, EM 17, to the pink filaments.

L62 ANSWER 74 OF 74 MEDLINE DUPLICATE 33
AB The 16S rRNA of the bacterion **Aquifex pyrophilus**, a microaerophilic, oxygen-reducing hyperthermophile, has been **sequenced** directly from the the PCR amplified gene. Phylogenetic analyses show the Aq. pyrophilus lineage to be probably the deepest (earliest) in the (eu)bacterial tree. The addition of this deep branching to the bacterial tree further supports the argument that the Bacteria are of thermophilic ancestry.

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